Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-133. (Canceled)

134. (Currently Amended) A process for delaying, repressing or otherwise reducing the expression of a target gene in a mammalian cell comprising introducing into a cell a double-stranded DNA construct consisting of a promoter operable in the cell, a transcription termination sequence active in the cell, and operably connected thereto

a first structural gene sequence comprising 20-30 consecutive nucleotides identical in sequence to a region of a target gene in the mammalian cell;

a second structural gene sequence comprising 20-30 consecutive nucleotides identical in sequence to, and in an inverted orientation relative to, the 20-30 consecutive nucleotides of the first structural gene sequence, thereby providing a repeating sequence which is only 20-30 consecutive nucleotides in length; and

a stuffer fragment which separates and links the first and second structural gene sequences,

such that the double-stranded DNA construct is transcribed to produce ~~the~~ a RNA molecule.

135. (Previously presented) The process of claim 134, wherein the region of the target gene is in an exon.

136. (Previously presented) The process of claim 134, wherein the target gene is a viral gene.

137. (Previously presented) The process of claim 136, wherein the viral gene encodes a DNA polymerase, RNA polymerase, or viral coat protein.

138. (Previously presented) The process of claim 134, wherein the target gene is from a lentivirus.

139. (Previously presented) The process of claim 134, wherein the target gene is from an immunodeficiency virus.

140. (Previously presented) The process of claim 134, wherein the target gene is from a single-stranded (+) RNA virus.

141. (Previously presented) The process of claim 134, wherein the target gene is from a double-stranded DNA virus.

142. (Previously presented) The process of claim 134, wherein the target gene is a transgene in the mammalian cell.

143. (Previously presented) The process of claim 134, wherein the target gene is an endogenous gene in the mammalian cell.

144. (Previously presented) The process of claim 134, wherein the 20-30 consecutive nucleotides are identical to a coding region of the target gene.

145. (Previously presented) The process of claim 134, wherein the 20-30 consecutive nucleotides are identical to a 5′- or 3′-untranslated sequence of the target gene.

146. (Previously Presented) The process of claim 134 wherein the first structural gene sequence, the stuffer fragment and the second structural gene sequence form an interrupted palindrome sequence, and wherein the repeating sequence of the interrupted palindrome sequence is only 20-30 consecutive nucleotides in length.

147. (Previously presented) The process of claim 146, wherein the stuffer fragment is a sequence of nucleotides 10-50 nucleotides in length.

148. (Previously presented) The process of claim 146, wherein the stuffer fragment is a sequence of nucleotides 50-100 nucleotides in length.

149. (Previously presented) The process of claim 146, wherein the stuffer fragment is a sequence of nucleotides 100-500 nucleotides in length.

150. (Currently Amended) The process of claim 134, wherein the double-stranded ~~synthetic gene~~ DNA construct is introduced by a virus particle.

151. (Currently Amended) The process of claim 134, wherein the double-stranded ~~synthetic gene~~ DNA construct is introduced by a liposome.

152. (Currently Amended) The process of claim 134, wherein the double-stranded ~~synthetic gene~~ DNA construct is introduced by transfection.

153. (Previously presented) The process of claim 134, wherein the cell is the mammalian cell.

154. (Currently Amended) The process of claim 134, wherein the double-stranded ~~synthetic gene~~ DNA construct is integrated into the genome of the cell.

155. (Currently Amended) A process for delaying, repressing or otherwise reducing the expression of a target gene in a mammalian cell comprising introducing into a cell a double-stranded DNA construct consisting of a promoter operable in the cell, a transcription termination sequence active in the cell, and operably connected thereto

a first structural gene sequence comprising 20-30 consecutive nucleotides identical in sequence to a region of a viral DNA polymerase gene, a viral RNA polymerase gene, a viral coat protein gene, or a visually-detectable gene involved in determining an external phenotype in the mammalian cell;

a second structural gene sequence comprising 20-30 consecutive nucleotides identical in sequence to, and in an inverted orientation relative to, the 20-30 consecutive nucleotides of the first structural gene sequence, thereby providing a repeating sequence which is only 20-30 consecutive nucleotides in length; and

a stuffer fragment which separates and links the first and second structural gene sequences,

wherein a repeating sequence within the double-stranded DNA construct is only 20-30 nucleotides in length,

such that the double-stranded DNA construct is transcribed to produce ~~the~~ a RNA molecule.

156. (New) The process of claim 134, wherein the first structural gene sequence consists of 20 consecutive nucleotides identical in sequence to a region of a target gene in the mammalian cell, and the second structural gene sequence consists of 20 consecutive nucleotides identical in sequence to, and in an inverted orientation relative to, the 20 consecutive nucleotides of the first structural gene sequence, thereby providing a repeating sequence which is only 20 consecutive nucleotides in length.

157. (New) The process of claim 155, wherein the first structural gene sequence consists of 20 consecutive nucleotides identical in sequence to a region of a viral DNA polymerase gene, a viral RNA polymerase gene, a viral coat protein gene, or a visually-detectable gene involved in determining an external phenotype in the mammalian cell, and the second structural gene sequence consists of 20 consecutive nucleotides identical in sequence to, and in an inverted orientation relative to, the 20 consecutive nucleotides of the first structural gene sequence, thereby providing a repeating sequence which is only 20 consecutive nucleotides in length.